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Sequence Listing was accepted with existing errors.

See attached Validation Report.

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217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Wed Jun 13 13:10:08 EDT 2007

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Application No: 10797262 Version No: 2.1

Input Set:

Output Set:

Started: 2007-06-13 13:09:59.493
Finished: 2007-06-13 13:10:00.325
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 832 ms
Total Warnings: 9
Total Errors: 1
No. of SeqIDs Defined: 11
Actual SeqID Count: 11

| Error code | Error Description |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (6) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (7) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (8) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (8) |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (10) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (11) |

SEQUENCE LISTING

<110> East Tennessee State University Research Foundation
Lampson, Bert
Veloire, Jashree

<120> RNA-DEPENDENT DNA POLYMERASE FROM GEOBACILLUS STEAROTHERMOPHILUS

<130> 2826067.000002

<140> 10/797,262

<141> 2004-03-10

<160> 11

<170> PatentIn version 3.3

<210> 1

<211> 1263

<212> DNA

<213> Geobacillus stearothermophilus

<220>

<221> CDS

<222> (1)..(1263)

<400> 1

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| Met Ala Leu Leu Glu Arg Ile Leu Ala Arg Asp Asn Leu Ile Thr Ala | |
| 1 5 10 15 | |

| | |
|---|----|
| ctc aaa cgg gtc gaa gcc aac caa gga gca ccg gga atc gac gga gta | 96 |
| Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile Asp Gly Val | |
| 20 25 30 | |

| | |
|---|-----|
| tca acc gat caa ctc cgt gat tac atc cgc gct cac tgg agc acg atc | 144 |
| Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile | |
| 35 40 45 | |

| | |
|---|-----|
| cgc gcc caa ctc ttg gcg gga acc tac cgg ccg gcg cct gtc cgc agg | 192 |
| Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg | |
| 50 55 60 | |

| | |
|---|-----|
| gtc gga atc ccg aaa ccg ggc ggc ggc aca cgg cag cta ggc att ccc | 240 |
| Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu Gly Ile Pro | |
| 65 70 75 80 | |

| | |
|---|-----|
| acc gtg gtg gac cgg ctg atc caa caa gcc att ctt caa gaa ctc aca | 288 |
| Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln Glu Leu Thr | |
| 85 90 95 | |

| | |
|---|-----|
| ccc att ttc gat cca gac ttc tcc cct tcc agc ttc gga ttc cgt ccg | 336 |
| Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro | |
| 100 105 110 | |

| | |
|---|-----|
| ggc cgt aac gcc cac gat gcc gtg cgg caa gcg caa ggc tac atc cag | 384 |
|---|-----|

| | |
|---|------|
| Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly Tyr Ile Gln | |
| 115 120 125 | |
| gaa ggg tat cgg tac gtg gtc gac atg gac ctg gaa aag ttc ttt gat | 432 |
| Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys Phe Phe Asp | |
| 130 135 140 | |
| cgg gtc aac cat gac atc ttg atg agt cgg gtg gcc cga aaa gtc aag | 480 |
| Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg Lys Val Lys | |
| 145 150 155 160 | |
| gat aaa cgc gtg ctg aaa ctg atc cgt gcc tac ctg caa gcc ggc gtt | 528 |
| Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln Ala Gly Val | |
| 165 170 175 | |
| atg atc gaa ggg gtg aag gtg cag acg gag gaa ggg acg ccg caa ggc | 576 |
| Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr Pro Gln Gly | |
| 180 185 190 | |
| ggc ccc ctc agc ccc ctg ctg gcg aac atc ctt ctc gac gat tta gac | 624 |
| Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp Asp Leu Asp | |
| 195 200 205 | |
| aag gaa ttg gag aag cga gga ttg aaa ttc tgc cgt tac gca gat gac | 672 |
| Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr Ala Asp Asp | |
| 210 215 220 | |
| tgc aac atc tat gtg aaa agt ctg cgg gca gga caa cgg gtg aaa caa | 720 |
| Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg Val Lys Gln | |
| 225 230 235 240 | |
| agc atc caa cgg ttc ttg gag aaa acg ctc aaa ctc aaa gta aac gag | 768 |
| Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys Val Asn Glu | |
| 245 250 255 | |
| gag aaa agt gcg gtg gac cgc ccg tgg aaa cgg gcc ttt ctg ggg ttt | 816 |
| Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe Leu Gly Phe | |
| 260 265 270 | |
| agc ttc aca ccg gaa cga aaa gcg cga atc cgg ctc gcc cca agg tcg | 864 |
| Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala Pro Arg Ser | |
| 275 280 285 | |
| att caa cgt ctg aaa cag cgg att cga cag ctg acc aac cca aac tgg | 912 |
| Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn Pro Asn Trp | |
| 290 295 300 | |
| agc ata tcg atg cca gaa cga att cat cgc gtc aat caa tac gtc atg | 960 |
| Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln Tyr Val Met | |
| 305 310 315 320 | |
| gga tgg atc ggg tat ttt cgg ctc gtc gaa acc ccg tct gtc ctt cag | 1008 |
| Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser Val Leu Gln | |
| 325 330 335 | |
| acc atc gaa gga tgg att cgg agg agg ctt cga ctc tgt caa tgg ctt | 1056 |
| Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys Gln Trp Leu | |

| 340 | 345 | 350 | |
|---|-----|-----|------|
| caa tgg aaa cgg gtc aga acc aga atc cgt gag tta aga gcg ctg ggg | | | 1104 |
| Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly | | | |
| 355 | 360 | 365 | |
| ctg aaa gag aca gcg gtg atg gag atc gcc aat acc cga aaa gga gct | | | 1152 |
| Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala | | | |
| 370 | 375 | 380 | |
| tgg cga aca acg aaa acg ccg caa ctc cac cag gcc ctg ggc aaa acc | | | 1200 |
| Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr | | | |
| 385 | 390 | 395 | 400 |
| tac tgg acc gct caa ggg ctc aag agt ttg acg caa cga tat ttc gaa | | | 1248 |
| Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu | | | |
| 405 | 410 | 415 | |
| ctc cgt caa ggt tga | | | 1263 |
| Leu Arg Gln Gly | | | |
| 420 | | | |
| | | | |
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| <211> 420 | | | |
| <212> PRT | | | |
| <213> <i>Geobacillus stearothermophilus</i> | | | |
| | | | |
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| Met Ala Leu Leu Glu Arg Ile Leu Ala Arg Asp Asn Leu Ile Thr Ala | | | |
| 1 | 5 | 10 | 15 |
| | | | |
| Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile Asp Gly Val | | | |
| 20 | 25 | 30 | |
| | | | |
| Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile | | | |
| 35 | 40 | 45 | |
| | | | |
| Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg | | | |
| 50 | 55 | 60 | |
| | | | |
| Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu Gly Ile Pro | | | |
| 65 | 70 | 75 | 80 |
| | | | |
| Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln Glu Leu Thr | | | |
| 85 | 90 | 95 | |
| | | | |
| Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro | | | |
| 100 | 105 | 110 | |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Asn | Ala | His | Asp | Ala | Val | Arg | Gln | Ala | Gln | Gly | Tyr | Ile | Gln | 115 | 120 | 125 |
| Glu | Gly | Tyr | Arg | Tyr | Val | Val | Asp | Met | Asp | Leu | Glu | Lys | Phe | Phe | Asp | 130 | 135 | 140 |
| Arg | Val | Asn | His | Asp | Ile | Leu | Met | Ser | Arg | Val | Ala | Arg | Lys | Val | Lys | 145 | 150 | 155 |
| Asp | Lys | Arg | Val | Leu | Lys | Leu | Ile | Arg | Ala | Tyr | Leu | Gln | Ala | Gly | Val | 165 | 170 | 175 |
| Met | Ile | Glu | Gly | Val | Lys | Val | Gln | Thr | Glu | Glu | Gly | Thr | Pro | Gln | Gly | 180 | 185 | 190 |
| Gly | Pro | Leu | Ser | Pro | Leu | Leu | Ala | Asn | Ile | Leu | Leu | Asp | Asp | Leu | Asp | 195 | 200 | 205 |
| Lys | Glu | Leu | Glu | Lys | Arg | Gly | Leu | Lys | Phe | Cys | Arg | Tyr | Ala | Asp | Asp | 210 | 215 | 220 |
| Cys | Asn | Ile | Tyr | Val | Lys | Ser | Leu | Arg | Ala | Gly | Gln | Arg | Val | Lys | Gln | 225 | 230 | 235 |
| Ser | Ile | Gln | Arg | Phe | Leu | Glu | Lys | Thr | Leu | Lys | Leu | Lys | Val | Asn | Glu | 245 | 250 | 255 |
| Glu | Lys | Ser | Ala | Val | Asp | Arg | Pro | Trp | Lys | Arg | Ala | Phe | Leu | Gly | Phe | 260 | 265 | 270 |
| Ser | Phe | Thr | Pro | Glu | Arg | Lys | Ala | Arg | Ile | Arg | Leu | Ala | Pro | Arg | Ser | 275 | 280 | 285 |
| Ile | Gln | Arg | Leu | Lys | Gln | Arg | Ile | Arg | Gln | Leu | Thr | Asn | Pro | Asn | Trp | 290 | 295 | 300 |
| Ser | Ile | Ser | Met | Pro | Glu | Arg | Ile | His | Arg | Val | Asn | Gln | Tyr | Val | Met | 305 | 310 | 315 |
| Gly | Trp | Ile | Gly | Tyr | Phe | Arg | Leu | Val | Glu | Thr | Pro | Ser | Val | Leu | Gln | 325 | 330 | 335 |

Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys Gln Trp Leu
340 345 350

Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly
355 360 365

Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala
370 375 380

Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr
385 390 395 400

Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu
405 410 415

Leu Arg Gln Gly
420

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<212> DNA
<213> Artificial

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<223> Plasmid construct

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<221> misc_feature
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aacgcatctt agcgagagac aacctcatca cggcgctcaa acgggtcgaa gccaaccaag 180
gagcaccggg aatcgacgga gtatcaaccg atcaactccg tgattacatc cgcgctcact 240
ggagcacgat ccgcgcccaa ctcttggcgg gaacctaccg gccggcgcct gtccgcaggg 300
tcggaatccc gaaaccgggc ggcggcacac ggcagctagg cattcccacc gtggtggacc 360
ggctgatcca acaagccatt cttcaagaac tcacacccat tttcgatcca gacttctccc 420
cttcagctt cggattccgt ccgggccgta acgcccacga tgccgtgcgg caagcgcaag 480
gtacatcca ggaagggtat cggtagctgg tcgacatgga cctggaaaag ttctttgatc 540

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gggtcaacca tgacatcttg atgagtcggg tggcccgaag agtcaaggat aaacgcgtgc 600
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cggaggaagg gacgcccga ggcggccccc tcagccccct gctggcgaac atccttctcg 720
acgatttaga caaggaattg gagaagcgag gattgaaatt ctgccgttac gcagatgact 780
gcaacatcta tgtgaaaagt ctgcgggcag gacaacgggt gaaacaaagc atccaacggt 840
tcttgagaaa aacgctcaaa ctcaaagtaa acgaggagaa aagtgcggtg gaccgcccgt 900
ggaaacgggc ctttctgggg tttagcttca caccggaacg aaaagcgcga atccggctcg 960
ccccaaggtc gattcaacgt ctgaaacagc ggattcgaca gctgaccaac ccaaactgga 1020
gcatatcgat gccagaacga attcatcgcg tcaatcaata cgtcatggga tggatcgggt 1080
atcttcggct cgtcgaaacc cgtctgtcc ttcagaccat cgaaggatgg attcggagga 1140
ggcttcgact ctgtcaatgg cttcaatgga aacgggtcag aaccagaatc cgtgagttaa 1200
gagcgtggg gctgaaagag acagcgggtga tggagatcgc caatacccg aaaggagctt 1260
ggcgaacaac gaaaacgcc caactccacc aggccctggg caaacctac tggaccgctc 1320
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<220>
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<222> (1)..(32)

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<210> 5
<211> 28
<212> DNA
<213> Artificial

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<220>
<223> Nucleotide primer containing BamHI restriction site

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<400> 5
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```


<210> 6
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<223> Nucleotide primer containing PstI restriction site

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<222> (1)..(29)

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<210> 7
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<223> Nucleotide primer containing HindIII restriction site

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<400> 7
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<212> PRT
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<220>
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<222> (1)..(455)

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1 5 10 15

| | | |
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| 20 | 25 | 30 |
| Lys Ile Thr Met Ala Leu Leu Glu Arg Ile Leu Ala Arg Asp Asn Leu | | |
| 35 | 40 | 45 |
| Ile Thr Ala Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile | | |
| 50 | 55 | 60 |
| Asp Gly Val Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp | | |
| 65 | 70 | 75 |
| Ser Thr Ile Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro | | |
| 85 | 90 | 95 |
| Val Arg Arg Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu | | |
| 100 | 105 | 110 |
| Gly Ile Pro Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln | | |
| 115 | 120 | 125 |
| Glu Leu Thr Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly | | |
| 130 | 135 | 140 |
| Phe Arg Pro Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly | | |
| 145 | 150 | 155 |
| Tyr Ile Gln Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys | | |
| 165 | 170 | 175 |
| Phe Phe Asp Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg | | |
| 180 | 185 | 190 |
| Lys Val Lys Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln | | |
| 195 | 200 | 205 |
| Ala Gly Val Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr | | |
| 210 | 215 | 220 |
| Pro Gln Gly Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp | | |
| 225 | 230 | 235 |
| | | 240 |

Asp Leu Asp Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr
245 250 255

Ala Asp Asp Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg
260 265 270

Val Lys Gln Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys
275 280 285

Val Asn Glu Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe
290 295 300

Leu Gly Phe Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala
305 310 315 320

Pro Arg Ser Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn
325 330 335

Pro Asn Trp Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln
340 345 350

Tyr Val Met Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser
355 360 365

Val Leu Gln Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys
370 375 380

Gln Trp Leu Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg
385 390 395 400

Ala Leu Gly Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg
405 410 415

Lys Gly Ala Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu
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Gly Lys Thr Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg
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Tyr Phe Glu Leu Arg Gln Gly
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<222> (1)..(25)

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